

WHAT WE CLAIM IS:

1. A method for identifying a compound for inducing apoptosis, comprising identifying an inhibitor of a target selected from the group consisting of: angi-associated, migratory cell protein (AAMP, comprising SEQ ID NO:2), a disintegrin and 5 metalloproteinase domain 8 (ADAM8, comprising SEQ ID NO:4), a disintegrin-like and metalloprotease (reporlysin type) with thrombospondin type 1 motif, 17 (ADAMTS17, comprising SEQ ID NO:6), adenylate cyclase 3 (ADCY3, comprising SEQ ID NO:8), adrenergic beta receptor kinase 1 (ADRBK1, comprising SEQ ID NO:10), bladder cancer associated protein (BLCAP, comprising SEQ ID NO:12), chromosome 22 open reading 10 frame 5 (C22orf5, comprising SEQ ID NO:14), CD81 antigen (target of antiproliferative antibody 1 (CD81, comprising SEQ ID NO:16), CD9 antigen (p24) (CD9, comprising SEQ ID NO:18), claudin 4 (CLDN4, comprising SEQ ID NO:20), chloride intracellular channel 1 (CLIC1, comprising SEQ ID NO:22), collagen, type VI, alpha 2 (COL6A2, comprising SEQ ID NO:24), CTL2 (CTL2, comprising SEQ ID NO:26), endothelin 15 converting enzyme 1 (ECE1, comprising SEQ ID NO:28), ephrin-B1 (EFNB1, comprising SEQ ID NO:30), flotillin 2 (FLOT2, comprising SEQ ID NO:32), intercellular adhesion molecule 3 (ICAM3, comprising SEQ ID NO:34), iduronate 2-sulfatase (Hunter syndrome) (IDS, comprising SEQ ID NO:36), jagged 2 (JAG2, comprising SEQ ID NO:38), junctional adhesion molecule 1 (JAM1, comprising SEQ ID 20 NO:40), lectin, galactoside-binding soluble 3 binding protein (LGALS3BP, comprising SEQ ID NO:42), similar to possible G-protein receptor (LOC146330, comprising SEQ ID NO:44), CGI-78 protein (LOC51107, comprising SEQ ID NO:46), lipoprotein lipase (LPL, comprising SEQ ID NO:48), low density lipoprotein receptor-related protein 5 (LRP5, comprising SEQ ID NO:50), Lutheran blood group (Auberger b antigen included) 25 (LU, comprising SEQ ID NO:52), membrane component, chromosome 11, surface marker 1 (M11S1, comprising SEQ ID NO:54), serum constituent protein (MSE55, comprising SEQ ID NO:56), neuropathy target esterase (NTE, comprising SEQ ID NO:58), Homo sapiens cDNA FL31043 fis, clone HSYRA2000248 (PLEXIN A1) or Homo sapiens cDNA FLJ44113 fis, clone TESTI4046487, highly similar to Mus 30 musculus plexin A1 (PLXNA1, comprising SEQ ID NO:60), protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein)(liprin), alpha 3

(PPFIA3, comprising SEQ ID NO:62), Homo sapiens peptide-histidine transporter 4 (PTR4), mRNA (PTR4, comprising SEQ ID NO:64), solute carrier family 16 (moncarboxylic acid transporters) member 3 (SLC16A3, comprising SEQ ID NO:66), solute carrier family 1 (neutral amino acid transporter) member 5 (SLC1A5, comprising SEQ ID NO:68), solute carrier family 39 (zinc transporter) member 3 (SLC39A1, comprising SEQ ID NO:70), serine protease inhibitor, Kunitz type 2 (SPINT2, comprising SEQ ID NO:72), stanniocalcin 2 (STC2, comprising SEQ ID NO:74), tumor necrosis receptor superfamily member 21 (TNFRSF21, comprising SEQ ID NO:76), tumor rejection antigen (gp96) 1 (TRA1, comprising SEQ ID NO:78), and transient receptor potential cation channel, subfamily M member 4 (TRPM4, comprising SEQ ID NO:80).

2. The method of Claim 1, further comprising assessing the ability of an identified inhibitor to induce apoptosis in a cell.

3. The method of Claim 2, further comprising detecting whether a compound identified as inducing apoptosis inhibits growth of tumor cells.

4. The method of Claim 1, wherein the step of identifying comprises identifying an inhibitor of expression or activity of the target.

5. The method of Claim 1, comprising the steps of:

a) contacting a host cell with a putative regulatory compound, wherein the host cell expresses the target or a biologically active fragment thereof; and

b) detecting whether the putative regulatory compound inhibits the target or biologically active fragment thereof, wherein a putative regulatory compound that inhibits the target as compared to in the absence of the compound is indicated to be a candidate compound for the induction of apoptosis in a host cell.

25 6. The method of Claim 5, wherein the host cell is a tumor cell line.

7. The method of Claim 5, wherein the step of detecting is selected from the group consisting of:

a) detecting expression of the target in the presence of the putative regulatory compound; and

30 b) detecting activity of the target in the presence of the putative regulatory compound.

8. The method of Claim 7, wherein the expression of the target is measured by polymerase chain reaction.

9. The method of Claim 7, wherein the expression of the target is measured using an antibody or antigen binding partner that selectively binds to the target.

5 10. The method of Claim 7, wherein the activity of the target is measured by measuring the amount of a product generated in a biochemical reaction mediated by the target.

10 11. The method of Claim 7, wherein the activity of the target is measured by measuring the amount of a substrate consumed in a biochemical reaction mediated by the target.

12. The method of Claim 1, comprising the steps of:

- a) determining the three-dimensional structure of the target;
- b) identifying the three-dimensional structure of a putative inhibitor by using computer software to model an interaction between the target structure and a structure of 15 a test compound; and
- c) synthesizing compounds identified in (b) and assaying the compounds in an *in vitro* assay to determine whether the compound inhibits the expression or activity of the target.

13. The method of Claim 1, wherein the target has been validated as being 20 involved in tumor cell growth.

14. The method of Claim 14, wherein the target has been validated as being involved in tumor cell growth by a process comprising:

- a) inhibiting the target in a cell by a method selected from the group consisting of gene knock-out, anti-sense oligonucleotide expression, use of RNAi 25 molecules and GSE expression; and
- b) assaying the cell for the ability of the cell to grow.

15. A method for inducing apoptosis, comprising inhibiting the expression or activity of a target or a gene encoding the target, wherein the target is selected from the group consisting of: angio-associated, migratory cell protein (AAMP, comprising SEQ ID NO:2), a disintegrin and metalloproteinase domain 8 (ADAM8, comprising SEQ ID NO:4), a disintegrin-like and metalloprotease (reporlysin type) with thrombospondin type 1 motif, 17 (ADAMTS17, comprising SEQ ID NO:6), adenylate cyclase 3 (ADCY3, comprising SEQ ID NO:8), adrenergic beta receptor kinase 1 (ADRBK1, comprising SEQ ID NO:10), bladder cancer associated protein (BLCAP, comprising SEQ ID NO:12), chromosome 22 open reading frame 5 (C22orf5, comprising SEQ ID NO:14), 10 CD81 antigen (target of antiproliferative antibody 1 (CD81, comprising SEQ ID NO:16), CD9 antigen (p24) (CD9, comprising SEQ ID NO:18), claudin 4 (CLDN4, comprising SEQ ID NO:20), chloride intracellular channel 1 (CLIC1, comprising SEQ ID NO:22), collagen, type VI, alpha 2 (COL6A2, comprising SEQ ID NO:24), CTL2 (CTL2, comprising SEQ ID NO:26), endothelin converting enzyme 1 (ECE1, comprising SEQ 15 ID NO:28), ephrin-B1 (EFNB1, comprising SEQ ID NO:30), flotillin 2 (FLOT2, comprising SEQ ID NO:32), intercellular adhesion molecule 3 (ICAM3, comprising SEQ ID NO:34), iduronate 2-sulfatase (Hunter syndrome) (IDS, comprising SEQ ID NO:36), jagged 2 (JAG2, comprising SEQ ID NO:38), junctional adhesion molecule 1 (JAM1, comprising SEQ ID NO:40), lectin, galactoside-binding soluble 3 binding protein 20 (LGALS3BP, comprising SEQ ID NO:42), similar to possible G-protein receptor (LOC146330, comprising SEQ ID NO:44), CGI-78 protein (LOC51107, comprising SEQ ID NO:46), lipoprotein lipase (LPL, comprising SEQ ID NO:48), low density lipoprotein receptor-related protein 5 (LRP5, comprising SEQ ID NO:50), Lutheran blood group (Auberger b antigen included) (LU, comprising SEQ ID NO:52), membrane component, 25 chromosome 11, surface marker 1 (M11S1, comprising SEQ ID NO:54), serum constituent protein (MSE55, comprising SEQ ID NO:56), neuropathy target esterase (NTE, comprising SEQ ID NO:58), Homo sapiens cDNA FL31043 fis, clone HSYRA2000248 (PLEXIN A1) or Homo sapiens cDNA FLJ44113 fis, clone TESTI4046487, highly similar to *Mus musculus* plexin A1 (PLXNA1, comprising SEQ 30 ID NO:60), protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein)(lpirin), alpha 3 (PPFIA3, comprising SEQ ID NO:62), Homo sapiens

peptide-histidine transporter 4 (PTR4), mRNA (PTR4, comprising SEQ ID NO:64),
solute carrier family 16 (moncarboxylic acid transporters) member 3 (SLC16A3,
comprising SEQ ID NO:66), solute carrier family 1 (neutral amino acid transporter)
member 5 (SLC1A5, comprising SEQ ID NO:68), solute carrier family 39 (zinc
5 transporter) member 3 (SLC39A1, comprising SEQ ID NO:70), serine protease inhibitor,
Kunitz type 2 (SPINT2, comprising SEQ ID NO:72), stanniocalcin 2 (STC2, comprising
SEQ ID NO:74), tumor necrosis receptor superfamily member 21 (TNFRSF21,
comprising SEQ ID NO:76), tumor rejection antigen (gp96) 1 (TRA1, comprising SEQ
ID NO:78), and transient receptor potential cation channel, subfamily M member 4
10 (TRPM4, comprising SEQ ID NO:80).

16. The method of Claim 15, wherein the step of inhibiting is conducted by
contacting a cell with an inhibitor of the target, wherein the inhibitor induces apoptosis in
the cell.

17. A method for the diagnosis of a tumor comprising:

a) detecting a level of expression or activity of at least one biomarker in a test sample from a patient to be diagnosed, wherein the biomarker is selected from the group consisting of: angio-associated, migratory cell protein (AAMP, comprising SEQ ID NO:2), a disintegrin and metalloproteinase domain 8 (ADAM8, comprising SEQ ID NO:4), a disintegrin-like and metalloprotease (reporlysin type) with thrombospondin type 1 motif, 17 (ADAMTS17, comprising SEQ ID NO:6), adenylate cyclase 3 (ADCY3, comprising SEQ ID NO:8), adrenergic beta receptor kinase 1 (ADRBK1, comprising SEQ ID NO:10), bladder cancer associated protein (BLCAP, comprising SEQ ID NO:12), chromosome 22 open reading frame 5 (C22orf5, comprising SEQ ID NO:14), CD81 antigen (target of antiproliferative antibody 1 (CD81, comprising SEQ ID NO:16), CD9 antigen (p24) (CD9, comprising SEQ ID NO:18), claudin 4 (CLDN4, comprising SEQ ID NO:20), chloride intracellular channel 1 (CLIC1, comprising SEQ ID NO:22), collagen, type VI, alpha 2 (COL6A2, comprising SEQ ID NO:24), CTL2 (CTL2, comprising SEQ ID NO:26), endothelin converting enzyme 1 (ECE1, comprising SEQ ID NO:28), ephrin-B1 (EFNB1, comprising SEQ ID NO:30), flotillin 2 (FLOT2, comprising SEQ ID NO:32), intercellular adhesion molecule 3 (ICAM3, comprising SEQ ID NO:34), iduronate 2-sulfatase (Hunter syndrome) (IDS, comprising SEQ ID NO:36), jagged 2 (JAG2, comprising SEQ ID NO:38), junctional adhesion molecule 1 (JAM1, comprising SEQ ID NO:40), lectin, galactoside-binding soluble 3 binding protein (LGALS3BP, comprising SEQ ID NO:42), similar to possible G-protein receptor (LOC146330, comprising SEQ ID NO:44), CGI-78 protein (LOC51107, comprising SEQ ID NO:46), lipoprotein lipase (LPL, comprising SEQ ID NO:48), low density lipoprotein receptor-related protein 5 (LRP5, comprising SEQ ID NO:50), Lutheran blood group (Auberger b antigen included) (LU, comprising SEQ ID NO:52), membrane component, chromosome 11, surface marker 1 (M11S1, comprising SEQ ID NO:54), serum constituent protein (MSE55, comprising SEQ ID NO:56), neuropathy target esterase (NTE, comprising SEQ ID NO:58), Homo sapiens cDNA FL31043 fis, clone HSYRA2000248 (PLEXIN A1) or Homo sapiens cDNA FLJ44113 fis, clone TESTI4046487, highly similar to *Mus musculus* plexin A1 (PLXNA1, comprising SEQ ID NO:60), protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF),

interacting protein)(liprin), alpha 3 (PPFIA3, comprising SEQ ID NO:62), Homo sapiens peptide-histidine transporter 4 (PTR4), mRNA (PTR4, comprising SEQ ID NO:64), solute carrier family 16 (moncarboxylic acid transporters) member 3 (SLC16A3, comprising SEQ ID NO:66), solute carrier family 1 (neutral amino acid transporter) 5 member 5 (SLC1A5, comprising SEQ ID NO:68), solute carrier family 39 (zinc transporter) member 3 (SLC39A1, comprising SEQ ID NO:70), serine protease inhibitor, Kunitz type 2 (SPINT2, comprising SEQ ID NO:72), stanniocalcin 2 (STC2, comprising SEQ ID NO:74), tumor necrosis receptor superfamily member 21 (TNFRSF21, comprising SEQ ID NO:76), tumor rejection antigen (gp96) 1 (TRA1, comprising SEQ 10 ID NO:78), and transient receptor potential cation channel, subfamily M member 4 (TRPM4, comprising SEQ ID NO:80);

15 b) comparing the level of expression or activity of the biomarker in the test sample to a baseline level of biomarker expression or activity established from a control sample; wherein detection of a statistically significant difference in the expression or activity of the biomarker in the test sample, as compared to the baseline level of the expression or biological activity of the biomarker, is an indicator of a difference in the tumorigenicity or potential therefore of cells in the patient.

18. The method of Claim 17, wherein the step of detecting comprises detecting biomarker mRNA transcription in the test sample.

20 19. The method of Claim 18, wherein the step of detecting is by a method selected from the group consisting of polymerase chain reaction (PCR), reverse transcriptase-PCR (RT-PCR), *in situ* hybridization, Northern blot, sequence analysis, gene microarray analysis, and detection of a reporter gene.

25 20. The method of Claim 17, wherein the step of detecting comprises detecting the biomarker protein in the test sample.

21. The method of Claim 20, wherein the step of detecting is by a method selected from the group consisting of immunoblot, enzyme-linked immunosorbant assay (ELISA), radioimmunoassay (RIA), immunoprecipitation, immunohistochemistry and immunofluorescence.

30 22. The method of Claim 17, wherein the step of detecting comprises detecting biomarker biological activity in the test sample.

23. The method of Claim 17, wherein detection of a statistically significant difference in the level of biomarker expression or activity in the test sample as compared to the baseline level, with a confidence of $p<0.05$, indicates that the cells in the test sample have a difference in tumorigenicity or potential therefore as compared to the 5 control sample.

24. The method of Claim 17, wherein the test sample is from a patient being diagnosed for cancer and wherein the baseline level is established from a control sample that is established as non-tumorigenic.

25. The method of Claim 24, wherein an increase in the level of biomarker 10 expression or activity of the test sample as compared to the baseline level of expression or activity indicates that cells from which the test sample was derived are predicted to be tumorigenic or predisposed to becoming tumorigenic.

26. The method of Claim 17, wherein the test sample is from a patient who is known to have cancer, and wherein the baseline level comprises a level of biomarker 15 expression or activity from a previous tumor cell sample from the patient;

wherein a statistically significant decrease in the level of biomarker expression or activity in the test sample as compared to the first baseline level of expression or activity from the previous tumor cell sample, indicates that the test sample is less tumorigenic than the previous tumor cell sample;

20 and wherein a statistically significant increase in the level of biomarker expression or activity in the test sample as compared to the first baseline level of expression or activity, indicates that the test sample is more tumorigenic than the previous tumor cell sample.

27. The method of Claim 26, wherein the method further comprises a step (c) 25 of modifying cancer treatment for the patient based on whether an increase or decrease in tumorigenicity is indicated in step (b).

28. The method of Claim 17, wherein the baseline level is established by a method selected from the group consisting of:

30 (1) establishing a baseline level of biomarker expression or activity in an autologous control sample from the patient, wherein the autologous sample is from a same cell type, tissue type or bodily fluid type as the test sample of step (a);

(2) establishing a baseline level of biomarker expression or activity from at least one previous detection of biomarker expression or activity in a previous test sample from the patient, wherein the previous test sample was of a same cell type, tissue type or bodily fluid type as the test sample of step (a); and

5 (3) establishing a baseline level of biomarker expression or activity from an average of control samples of a same cell type, tissue type or bodily fluid type as the test sample of step (a), the control samples having been obtained from a population of matched individuals.

29. The method of Claim 17, wherein the patient test sample is immobilized
10 on a substrate.

30. The method of Claim 17, wherein the test sample is a bodily fluid sample.

31. The method of Claim 17, wherein the biomarker level is determined by contacting the patient test sample with an antibody or a fragment thereof that selectively binds specifically to the biomarker, and determining whether the antibody or fragment
15 thereof has bound to the marker.

32. The method of Claim 17, wherein the method is used to determine the prognosis for cancer in the patient.

33. The method of Claim 17, wherein the method is used to determine the susceptibility of the patient to a therapeutic treatment.